```
<!--StartFragment-->RESULT 5
BH789726/c
LOCUS       BH789726                65 bp    DNA       linear   GSS 02-APR-2002
DEFINITION  SALK_044532.19.55.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_044532.19.55.x, genomic
            survey sequence.
ACCESSION   BH789726
VERSION     BH789726.1  GI:19882824
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 65)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within an annotated exon of At3g41627.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /ecotype="Col-0"
                     /db_xref="taxon:3702"
                     /clone="SALK_044532.19.55.x"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
ORIGIN

  Query Match          100.0%;  Score 12;  DB 15;  Length 65;
  Best Local Similarity  100.0%;  Pred. No. 3.7e+04;
  Matches  12;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;


Qy          1 GCCAGCGGAGTC 12
              ||||||||||||
Db         21 GCCAGCGGAGTC 10

<!--EndFragment-->
```